

# SEQUENCE LISTING

<110> Sanders, Bob G.  
Kline, Kimberly  
Yu, Weiping  
Liu, Hui  
Hantash, Feras

<120> Tocopherol Associated Protein and Uses Thereof

<130> D6453CIP

<141> 2003-10-29  
<150> US 10/419,629  
<151> 2003-04-21

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| caagccagaa  | gcttcgacct  | gcagaagtcg | gaggccatgc | tccggaagca  | 100  |
| tgtggagttc  | cgaaagcaaa  | aggacattga | caacatcatt | agcatggcag  | 150  |
| cctccagagg  | tgatccaaca  | gtatctgtca | ctggatgcc  | agggctctgct | 200  |
| gttctcagcc  | tccaaacagg  | acctgctgag | gaccaagatg | ctggatgcc   | 250  |
| agggctctgct | gttctcagcc  | tccaaacagg | acctgctgag | gaccaagatg  | 300  |
| cgggagtggt  | agctgcttct  | gcaagagtgt | gcccaccaga | ccacaaagtt  | 350  |
| ggggaggaag  | gtggagacca  | tcaccataat | ttatgactgc | gaggggcttg  | 400  |
| gcctcaagca  | tctctggaag  | cctgctgtgg | aggcctatgg | agagttttctc | 450  |
| tgcattgtttg | aggaaaatta  | tcccgaataa | ctgaagcgtc | tttttggtgt  | 500  |
| taaagccccc  | aaactgtttc  | ctgtggccta | taacctcatc | aaacccttcc  | 550  |
| tgagtgaaga  | cactcgtaag  | aagatcatgg | tcctgggagc | aaattggaag  | 600  |
| gaggtttttac | tgaaacatat  | cagccctgac | caggtgcctg | tggagtattg  | 650  |
| gggcgccatg  | actgaccctg  | atggaaaacc | caagtgcaaa | tccaagatca  | 700  |
| actacggggg  | tgacatcccc  | aggaagtatt | atgtgcgaga | ccaggtgaaa  | 750  |
| cagcagtatg  | aacacagcgt  | gcagatttcc | cgtggctcct | cccaccaagt  | 800  |
| ggagtatgag  | atcctcttcc  | ctggctgtgt | cctcaggtgg | cagtttatgt  | 850  |
| cagatggagc  | ggatgttggt  | tttgggattt | tcctgaagac | caagatggga  | 900  |
| gagaggcagc  | gggcagggga  | gatgacagag | gtgctgcccc | accagaggta  | 950  |
| caactcccac  | ctggtcccctg | aagatgggac | cctcacctgc | agtgatcctg  | 1000 |
| gcattctatgt | cctgcggttt  | gacaacacct | acagcttcat | tcatgccaaag | 1050 |
| aaggtcaatt  | tactgtgga   | ggtcctgctt | ccagacaaag | cctcagaaga  | 1100 |
| gaagatgaaa  | cagctggggg  | caggcacccc | gaaataa    |             | 1137 |

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 <223> TAP-38 polypeptide

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 Ser Gly Ser Met Trp Ser Ser Glu Ser Lys Arg Thr Leu Thr Thr  
                   35                  40                  45  
 Ser Leu Ala Trp Gln Pro Pro Glu Val Ile Gln Gln Tyr Leu Ser  
                   50                  55                  60  
 Gly Gly Met Cys Gly Tyr Asp Leu Asp Gly Cys Pro Val Trp Tyr  
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 Asp Ile Ile Gly Pro Lys Asp Ala Lys Gly Leu Leu Phe Ser Ala  
                   80                  85                  90  
 Ser Lys Gln Asp Leu Leu Arg Thr Lys Met Arg Glu Cys Glu Leu  
                   95                  100                 105  
 Leu Leu Gln Glu Cys Ala His Gln Thr Thr Lys Leu Gly Arg Lys  
                  110                 115                 120  
 Val Glu Thr Ile Thr Ile Ile Tyr Asp Cys Glu Gly Leu Gly Leu  
                  125                 130                 135  
 Lys His Leu Trp Lys Pro Ala Val Glu Ala Tyr Gly Glu Phe Leu  
                  140                 145                 150  
 Cys Met Phe Glu Glu Asn Tyr Pro Glu Thr Leu Lys Arg Leu Phe  
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 Val Val Lys Ala Pro Lys Leu Phe Pro Val Ala Tyr Asn Leu Ile  
                  170                 175                 180  
 Lys Pro Phe Leu Ser Glu Asp Thr Arg Lys Lys Ile Met Val Leu  
                  185                 190                 195  
 Gly Ala Asn Tyr Lys Glu Val Leu Leu Lys His Ile Ser Pro Asp  
                  200                 205                 210  
 Gln Val Pro Val Glu Tyr Gly Gly Thr Met Thr Asp Pro Asp Gly  
                  215                 220                 225  
 Asn Pro Lys Cys Lys Ser Lys Ile Asn Tyr Gly Gly Asp Ile Pro  
                  230                 235                 240  
 Arg Lys Tyr Tyr Val Arg Asp Gln Val Lys Gln Gln Tyr Glu His  
                  245                 250                 255  
 Ser Val Gln Ile Ser Arg Gly Ser Ser His Gln Val Glu Tyr Glu  
                  260                 265                 270  
 Ile Leu Phe Pro Gly Cys Val Leu Arg Trp Gln Phe Met Ser Asp  
                  275                 280                 285  
 Gly Ala Asp Val Gly Phe Gly Ile Phe Leu Lys Thr Lys Met Gly  
                  290                 295                 300  
 Glu Arg Gln Arg Ala Gly Glu Met Thr Glu Val Leu Pro Asn Gln  
                  305                 310                 315  
 Arg Tyr Asn Ser His Leu Val Pro Glu Asp Gly Thr Leu Thr Cys

|                 |                     |                     |     |  |     |
|-----------------|---------------------|---------------------|-----|--|-----|
|                 | 320                 |                     | 325 |  | 330 |
| Ser Asp Pro Gly | Ile Tyr Val Leu Arg | Phe Asp Asn Thr Tyr | Ser |  |     |
|                 | 335                 |                     | 340 |  | 345 |
| Phe Ile His Ala | Lys Lys Val Asn Phe | Thr Val Glu Val Leu | Leu |  |     |
|                 | 350                 |                     | 355 |  | 360 |
| Pro Asp Lys Ala | Ser Glu Glu Lys Met | Lys Gln Leu Gly Ala | Gly |  |     |
|                 | 365                 |                     | 370 |  | 375 |
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| caagtttcgg  | gagaatgtcc | aggatgtgct  | gccggccctg  | ccgaatccag  | 100  |
| atgactatatt | tctcctgcgt | tggctccgag  | ccagaagctt  | cgacctgcag  | 150  |
| aagtcggagg  | ccatgctccg | gaagcatgtg  | gagttccgaa  | agcaaaaagga | 200  |
| cattgacaac  | atcattagct | ggcagcctcc  | agaggtgatc  | caacagtatc  | 250  |
| tgtcactgga  | tgccaagggt | ctgctgttct  | cagcctccaa  | acaggacctg  | 300  |
| ctgaggacca  | agatgctgga | tgccaagggt  | ctgctgttct  | cagcctccaa  | 350  |
| acaggacctg  | ctgaggacca | agatgcggga  | gtgtgagctg  | cttctgcaag  | 400  |
| agtgtgcccc  | ccagaccaca | aagttgggga  | ggaagggtgga | gaccatcacc  | 450  |
| ataatttatg  | actgcgaggg | gcttggcctc  | aagcatctct  | ggaagcctgc  | 500  |
| tgtggaggcc  | tatggagagt | ttctctgcat  | gtttgaggaa  | aattatcccg  | 550  |
| aaacactgaa  | gcgtcttttt | gttggttaaag | cccccaaact  | gtttcctgtg  | 600  |
| gcctataaacc | tcatcaaacc | cttcctgagt  | gaggacactc  | gtaagaagat  | 650  |
| catggtcctg  | ggagcaaatt | ggaaggaggt  | tttactgaaa  | catatcagcc  | 700  |
| ctgaccaggt  | gcctgtggag | tatgggggcg  | ccatgactga  | ccctgatgga  | 750  |
| aaccccaagt  | gcaaatccaa | gatcaactac  | gggggtgaca  | tccccaggaa  | 800  |
| gtattatgtg  | cgagaccagg | tgaaacagca  | gtatgaacac  | agcgtgcaga  | 850  |
| tttcccgtgg  | ctcctcccac | caagtggagt  | atgagatcct  | cttccctggc  | 900  |
| tgtgtcctca  | ggtggcagtt | tatgtcagat  | ggagcggatg  | ttggtttttg  | 950  |
| gattttcctg  | aagaccaaga | tgaggagagag | gcagcgggca  | ggggagatga  | 1000 |
| cagaggtgct  | gccaaccag  | aggtacaact  | cccacctggt  | ccctgaagat  | 1050 |
| gggaccctca  | cctgcagtga | tcctggcatc  | tatgtcctgc  | ggtttgacaa  | 1100 |
| cacctacagc  | ttcattcatg | ccaagaaggt  | caatttcact  | gtggaggtcc  | 1150 |
| tgcttccaga  | caaagcctca | gaagagaaga  | tgaaacagct  | gggggcaggc  | 1200 |
| accccgaaat  | aa         |             |             |             | 1212 |

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<223> TAP-46 polypeptide

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| Met Ser Gly Arg Val Gly Asp Leu Ser Pro Arg Gln Lys Glu Ala | 5 10 15     |  |
| Leu Ala Lys Phe Arg Glu Asn Val Gln Asp Val Leu Pro Ala Leu | 20 25 30    |  |
| Pro Asn Pro Asp Asp Tyr Phe Leu Leu Arg Trp Leu Arg Ala Arg | 35 40 45    |  |
| Ser Phe Asp Leu Gln Lys Ser Glu Ala Met Leu Arg Lys His Val | 50 55 60    |  |
| Glu Phe Arg Lys Gln Lys Asp Ile Asp Asn Ile Ile Ser Trp Gln | 65 70 75    |  |
| Pro Pro Glu Val Ile Gln Gln Tyr Leu Ser Gly Gly Met Cys Gly | 80 85 90    |  |
| Tyr Asp Leu Asp Gly Cys Pro Val Trp Tyr Asp Ile Ile Gly Pro | 95 100 105  |  |
| Leu Asp Ala Lys Gly Leu Leu Phe Ser Ala Ser Lys Gln Asp Leu | 110 115 120 |  |
| Leu Arg Thr Lys Met Arg Glu Cys Glu Leu Leu Leu Gln Glu Cys | 125 130 135 |  |
| Ala His Gln Thr Thr Lys Leu Gly Arg Lys Val Glu Thr Ile Thr | 140 145 150 |  |
| Ile Ile Tyr Asp Cys Glu Gly Leu Gly Leu Lys His Leu Trp Lys | 155 160 165 |  |
| Pro Ala Val Glu Ala Tyr Gly Glu Phe Leu Cys Met Phe Glu Glu | 170 175 180 |  |
| Asn Tyr Pro Glu Thr Leu Lys Arg Leu Phe Val Val Lys Ala Pro | 185 190 195 |  |
| Lys Leu Phe Pro Val Ala Tyr Asn Leu Ile Lys Pro Phe Leu Ser | 200 205 210 |  |
| Glu Asp Thr Arg Lys Lys Ile Met Val Leu Gly Ala Asn Trp Lys | 215 220 225 |  |
| Glu Val Leu Leu Lys His Ile Ser Pro Asp Gln Val Pro Val Glu | 230 235 240 |  |
| Tyr Gly Gly Thr Met Thr Asp Pro Asp Gly Asn Pro Lys Cys Lys | 245 250 255 |  |
| Ser Lys Ile Asn Tyr Gly Gly Asp Ile Pro Arg Lys Tyr Tyr Val | 260 265 270 |  |
| Arg Asp Gln Val Lys Gln Gln Tyr Glu His Ser Val Gln Ile Ser | 275 280 285 |  |
| Arg Gly Ser Ser His Gln Val Glu Tyr Glu Ile Leu Phe Pro Gly | 290 295 300 |  |
| Cys Val Leu Arg Trp Gln Phe Met Ser Asp Gly Ala Asp Val Gly | 305 310 315 |  |
| Phe Gly Ile Phe Leu Lys Thr Lys Met Gly Glu Arg Gln Arg Ala | 320 325 330 |  |
| Gly Glu Met Thr Glu Val Leu Pro Asn Gln Arg Tyr Asn Ser His | 335 340 345 |  |
| Leu Val Pro Glu Asp Gly Thr Leu Thr Cys Ser Asp Pro Gly Ile | 350 355 360 |  |
| Tyr Val Leu Arg Phe Asp Asn Thr Tyr Ser Phe Ile His Ala Lys |             |  |

|                     |                     |                     |     |
|---------------------|---------------------|---------------------|-----|
| Lys Val Asn Phe     | 365                 | 370                 | 375 |
| Thr Val Glu Val Leu |                     | Leu Pro Asp Lys Ala | Ser |
|                     | 380                 | 385                 | 390 |
| Glu Glu Lys Met     | Lys Gln Leu Gly Ala | Gly Thr Pro Lys     |     |
|                     | 395                 | 400                 |     |

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 cggcgat 57

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 <223> 16 amino acids from the c-terminus of TAP attached  
 to keyhole limpet hemocyanin

<400> 8



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 <213> *Homo sapiens*

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 <223> deletion mutant TAP-882

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 ggaaggtgga gaccatcacc ataatttatg actgcgaggg gcttggcctc 150  
 aagcatctct ggaagcctgc tgtggaggcc tatggagagt ttctctgcat 200  
 gtttgaggaa aattatcccc aaacactgaa gcgtcttttt gttgttaaag 250  
 cccccaaact gtttcctgtg gcctataacc tcatcaaacc ctccctgagt 300  
 gaggacactc gtaagaagat catggtcctg ggagcaaatt ggaaggaggt 350  
 tttactgaaa catatcagcc ctgaccaggt gcctgtggag tatgggggca 400  
 ccatgactga ccctgatgga aaccccaagt gcaaatacaa gatcaactac 450  
 ggggggtgaca tccccaggaa gtattatgtg cgagaccagg tgaaacagca 500  
 gtatgaacac agcgtgcaga tttcccgtgg ctccctccac caagtggagt 550  
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 ggagcggatg ttggttttgg gattttcctg aagaccaaga tgggagagag 650  
 gcagcgggca ggggagatga cagaggtgct gcccaaccag aggtacaact 700  
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 tatgtcctgc ggtttgacaa cacctacagc ttcattcatg ccaagaaggt 800  
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<220>  
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| Arg Glu Cys Glu Leu Leu Leu Gln Glu Cys Ala His Gln Thr Thr | 20  | 25  |
| Lys Leu Gly Arg Lys Val Glu Thr Ile Thr Ile Ile Tyr Asp Cys | 35  | 40  |
| Glu Gly Leu Gly Leu Lys His Leu Trp Lys Pro Ala Val Glu Ala | 50  | 55  |
| Tyr Gly Glu Phe Leu Cys Met Phe Glu Glu Asn Tyr Pro Glu Thr | 65  | 70  |
| Leu Lys Arg Leu Phe Val Val Lys Ala Pro Lys Leu Phe Pro Val | 80  | 85  |
| Ala Tyr Asn Leu Ile Lys Pro Phe Leu Ser Glu Asp Thr Arg Lys | 95  | 100 |
| Lys Ile Met Val Leu Gly Ala Asn Trp Lys Glu Val Leu Leu Lys | 110 | 115 |
| His Ile Ser Pro Asp Gln Val Pro Val Glu Tyr Gly Gly Thr Met | 125 | 130 |
| Thr Asp Pro Asp Gly Asn Pro Lys Cys Lys Ser Lys Ile Asn Tyr | 140 | 145 |
| Gly Gly Asp Ile Pro Arg Lys Tyr Tyr Val Arg Asp Gln Val Lys | 155 | 160 |
| Gln Gln Tyr Glu His Ser Val Gln Ile Ser Arg Gly Ser Ser His | 170 | 175 |
| Gln Val Glu Tyr Glu Ile Leu Phe Pro Gly Cys Val Leu Arg Trp | 185 | 190 |
| Gln Phe Met Ser Asp Gly Ala Asp Val Gly Phe Gly Ile Phe Leu | 200 | 205 |
| Lys Thr Lys Met Gly Glu Arg Gln Arg Ala Gly Glu Met Thr Glu | 215 | 220 |
| Val Leu Pro Asn Gln Arg Tyr Asn Ser His Leu Val Pro Glu Asp | 230 | 235 |
| Gly Thr Leu Thr Cys Ser Asp Pro Gly Ile Tyr Val Leu Arg Phe | 245 | 250 |
| Asp Asn Thr Tyr Ser Phe Ile His Ala Lys Lys Val Asn Phe Thr | 260 | 265 |
| Val Glu Val Leu Leu Pro Asp Lys Ala Ser Glu Glu Lys Met Lys | 275 | 280 |
| Gln Leu Gly Ala Gly Thr Pro Lys                             | 290 | 293 |

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 <213> *Homo sapiens*

<220>  
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 <223> deletion mutant TAP-681



<400> 16

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aggacactcg taagaagatc atggctcctgg gagcaaattg gaaggagggt 150
ttactgaaac atatcagccc tgaccagggtg cctgtggagt atggggggcac 200
catgactgac cctgatggaa accccaagtg caaatccaag atcaactacg 250
ggggtgacat ccccgaggag tattatgtgc gagaccagggt gaaacagcag 300
tatgaacaca gcgtgcagat ttcccgtggc tcctcccacc aagtggagta 350
tgagatcctc ttccctggct gtgtcctcag gtggcagttt atgtcagatg 400
gagcggatgt tgggttttggg attttcctga agaccaagat gggagagagg 450
cagcgggcag gggagatgac agagggtgctg cccaaccaga ggtacaactc 500
ccacctggtc cctgaagatg ggaccctcac ctgcagtgat cctggcatct 550
atgtcctgcg gtttgacaac acctacagct tcattcatgc caagaaggctc 600
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gaaacagctg ggggcaggca ccccgaaata a 681

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 <220>  
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<400> 17

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      20      25      30
Phe Leu Ser Glu Asp Thr Arg Lys Lys Ile Met Val Leu Gly Ala
      35      40      45
Asn Trp Lys Glu Val Leu Leu Lys His Ile Ser Pro Asp Gln Val
      50      55      60
Pro Val Glu Tyr Gly Gly Thr Met Thr Asp Pro Asp Gly Asn Pro
      65      70      75
Lys Cys Lys Ser Lys Ile Asn Tyr Gly Gly Asp Ile Pro Arg Lys
      80      85      90
Tyr Tyr Val Arg Asp Gln Val Lys Gln Gln Tyr Glu His Ser Val
      95     100     105
Gln Ile Ser Arg Gly Ser Ser His Gln Val Glu Tyr Glu Ile Leu
     110     115     120
Phe Pro Gly Cys Val Leu Arg Trp Gln Phe Met Ser Asp Gly Ala
     125     130     135
Asp Val Gly Phe Gly Ile Phe Leu Lys Thr Lys Met Gly Glu Arg
     140     145     150
Gln Arg Ala Gly Glu Met Thr Glu Val Leu Pro Asn Gln Arg Tyr
     155     160     165
Asn Ser His Leu Val Pro Glu Asp Gly Thr Leu Thr Cys Ser Asp
     170     175     180
Pro Gly Ile Tyr Val Leu Arg Phe Asp Asn Thr Tyr Ser Phe Ile
     185     190     195
His Ala Lys Lys Val Asn Phe Thr Val Glu Val Leu Leu Pro Asp

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Ser | Glu | Glu | Lys | Met | Lys | Gln | Leu | Gly | Ala | Gly | Thr | Pro |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |
| Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
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 gtggctcctc ccaccaagtg gagtatgaga tcctcttccc tggctgtgtc 150  
 ctcaggtggc agtttatgtc agatggagcg gatgttggtt ttgggatttt 200  
 cctgaagacc aagatgggag agaggcagcg ggcaggggag atgacagagg 250  
 tgctgcccac ccagaggtac aactcccacc tggtcctga agatgggacc 300  
 ctcacctgca gtgatcctgg catctatgtc ctgcggtttg acaacaccta 350  
 cagcttcatt catgccaaga aggtcaattt cactgtggag gtcctgcttc 400  
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 aaataa 456

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 <212> PRT  
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 20 25 30  
 Gln Ile Ser Arg Gly Ser Ser His Gln Val Glu Tyr Glu Ile Leu  
 35 40 45  
 Phe Pro Gly Cys Val Leu Arg Trp Gln Phe Met Ser Asp Gly Ala  
 50 55 60  
 Asp Val Gly Phe Gly Ile Phe Leu Lys Thr Lys Met Gly Glu Arg  
 65 70 75  
 Gln Arg Ala Gly Glu Met Thr Glu Val Leu Pro Asn Gln Arg Tyr  
 80 85 90  
 Asn Ser His Leu Val Pro Glu Asp Gly Thr Leu Thr Cys Ser Asp  
 95 100 105  
 Pro Gly Ile Tyr Val Leu Arg Phe Asp Asn Thr Tyr Ser Phe Ile  
 110 115 120

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Ala | Lys | Lys | Val | Asn | Phe | Thr | Val | Glu | Val | Leu | Leu | Pro | Asp |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |
| Lys | Ala | Ser | Glu | Glu | Lys | Met | Lys | Gln | Leu | Gly | Ala | Gly | Thr | Pro |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |
| Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 151 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |